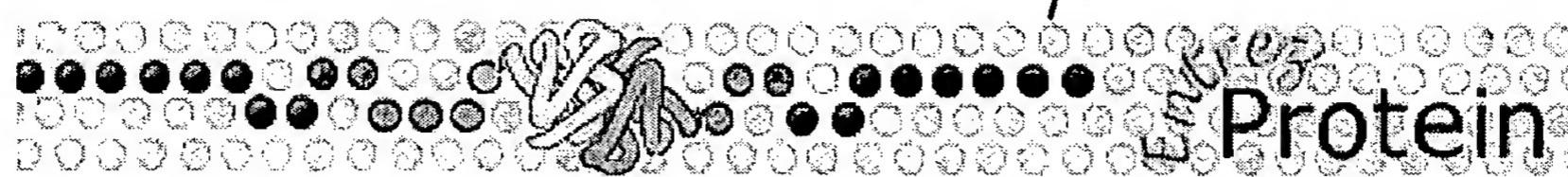




Appendix A

APPLICANTS
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Protein

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 1: Q15012. Lysosomal-associa...[gi:3122413]
[BLINK, Domains, Links](#)

LOCUS Q15012 233 aa linear PRI 15-MAR-2004

DEFINITION Lysosomal-associated transmembrane protein 4A (Golgi 4-transmembrane spanning transporter MTP).

ACCESSION Q15012

VERSION Q15012 GI:3122413

DBSOURCE swissprot: locus MTRP_HUMAN, accession Q15012; class: standard.
created: Jul 15, 1998.
sequence updated: Jul 15, 1998.
annotation updated: Mar 15, 2004.

xrefs: gi: [285962](#), gi: [40788948](#), gi: [33875421](#), gi: [12653305](#)
xrefs (non-sequence databases): GenewHGNC:6924, InterProIPR004687, PfamPF03821, TIGRFAMsTIGR00799

KEYWORDS Transmembrane; Transport.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (residues 1 to 233)

AUTHORS Nagase,T., Miyajima,N., Tanaka,A., Sazuka,T., Seki,N., Sato,S., Tabata,S., Ishikawa,K.-I., Kawarabayasi,Y., Kotani,H. and Nomura,N.

TITLE Prediction of the coding sequences of unidentified human genes. III. The coding sequences of 40 new genes (KIAA0081-KIAA0120) deduced by analysis of cDNA clones from human cell line KG-1 DNA Res. 2 (1), 37-43 (1995)

JOURNAL [95308325](#)

MEDLINE [7788527](#)

PUBMED

REMARK SEQUENCE FROM N.A.
TISSUE=Bone marrow

REFERENCE 2 (residues 1 to 233)

AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S.N., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnurch,A., Schein,J.E., Jones,S.J.M. and Marra,M.A.

TITLE Generation and initial analysis of more than 15,000 full-length

JOURNAL human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
MEDLINE 22388257
PUBMED 12477932
REMARK SEQUENCE FROM N.A.
TISSUE=Muscle
COMMENT -----
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[FUNCTION] May function in the transport of nucleosides and/or nucleoside derivatives between the cytosol and the lumen of an intracellular membrane-bound compartment (By similarity).
[SUBCELLULAR LOCATION] Integral membrane protein. May reside in an intracellular membrane-bound compartment (Potential).
[DOMAIN] The C-terminal domain is necessary for retention within intracellular membranes (By similarity).
FEATURES Location/Qualifiers
source 1..233
/organism="Homo sapiens"
/db_xref="taxon:9606"
gene 1..233
/gene="LAPTM4A"
/note="synonyms: MTRP, KIAA0108"
Protein 1..233
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/product="Lysosomal-associated transmembrane protein 4A"
Region 29..49
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/region_name="Transmembrane region"
/note="Potential."
Region 82..102
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/region_name="Transmembrane region"
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Region 108..128
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Region 160..180
/gene="LAPTM4A"
/region_name="Transmembrane region"
/note="Potential."
Region 226..229
/gene="LAPTM4A"
/region_name="Domain"
/note="Poly-Pro."
ORIGIN
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121 vlsclvaiss ltylprikey ldqlpdfpyk ddllaldssc llfivlvffa lfiifkayli
181 ncvwnckyki nnrnvpelav ypafeappqy vlptyemavk mpekeppppp lpa
//